SEQUENCE LISTING

<110> Elliott, Steven G.
Rogers, Norma
Busse, Leigh Anne

<120> G-Protein Coupled Receptor Molecules and Uses Thereof

<130> 02-076

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<150> 60/269,040
<151> 2001-02-14

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<170> PatentIn Ver. 2.0

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Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
             20                  25                  30

aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag acc tgg aag   144
Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
         35                  40                  45

ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat ttc ctc ctt   192
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
     50                  55                  60

atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga cgt aga cac   240
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
 65                  70                  75                  80

tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc acg ttg gcc   288
Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
                 85                  90                  95

atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg gct gcg gac   336
Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
            100                 105                 110
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agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac act atc tcc   384
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
        115                 120                 125

acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc ctg gtc atc   432
Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
    130                 135                 140

ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc gtg caa gag   480
Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
145                 150                 155                 160

acg gcc gtc tcc tgt gag agc ttc atc atg gag tcg gcc aat ggc tgg   528
Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
                165                 170                 175

cat gac atc atg ttc cag ctg gag ttc ttt atg ccc ctc ggc atc atc   576
His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
            180                 185                 190

tta ttt tgc tcc ttc aag att gtt tgg agc ctg agg cgg agg cag cag   624
Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
        195                 200                 205

ctg gcc aga cag gct cgg atg aag aag gcg acc cgg ttc atc atg gtg   672
Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
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gtg gca att gtg ttc atc aca tgc tac ctg ccc agc gtg tct gct aga   720
Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
225                 230                 235                 240

ctc tat ttc ctc tgg acg gtg ccc tcg agt gcc tgc gat ccc tct gtc   768
Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
                245                 250                 255

cat ggg gcc ctg cac ata acc ctc agc ttc acc tac atg aac agc atg   816
His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
            260                 265                 270

ctg gat ccc ctg gtg tat tat ttt tca agc ccc tcc ttt ccc aaa ttc   864
Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
        275                 280                 285

tac aac aag ctc aaa atc tgc agt ctg aaa ccc aag cag cca gga cac   912
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
    290                 295                 300

tca aaa aca caa agg ccg gaa gag atg cca att tcg aac ctc ggt cgc   960
Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
305                 310                 315                 320

agg agt tgc atc agt gtg gca aat agt ttc caa agc cag tct gat ggg  1008
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
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caa tgg gat ccc cac att gtt gag tgg cac 1038
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35 40 45

Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
50 55 60

Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
65 70 75 80

Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
85 90 95

Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
100 105 110

Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
115 120 125

Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
130 135 140

Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
145 150 155 160

Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
165 170 175

His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
180 185 190

Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
195 200 205

Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
210 215 220

Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
225 230 235 240

Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val

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                245                 250                 255

His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
            260                 265                 270

Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
        275                 280                 285

Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
    290                 295                 300

Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
305                 310                 315                 320

Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
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Gln Trp Asp Pro His Ile Val Glu Trp His
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cgcttgcacc ccagagcctg acccagctgc aggcttcaac tctgtagggg acgtgcagct 180

cgtgatccaa gcctaggaga aaggacttgc tgccggcttt catttcctgg ctgaagtttc 240

tctcgtgggt gcagcgcctg catcccaggg tgatgaggtt aggggcccag ctgctagagg 300

agccctagtg ttcggatagg cagctgtgcc tctgtgccgg ccaccttgg atg cca gtc 358
                                                    Met Pro Val
                                                      1

ctc tct cca act gct atg gac aac ggg tcg tgc tgt ctc atc gag ggg   406
Leu Ser Pro Thr Ala Met Asp Asn Gly Ser Cys Cys Leu Ile Glu Gly
      5   10   15

gag ccc atc tcc cag gtg atg cct cct cta ctc atc ctg gtc ttc gtg   454
Glu Pro Ile Ser Gln Val Met Pro Pro Leu Leu Ile Leu Val Phe Val
 20   25   30   35

ctt ggc gcc ctg ggc aac ggc ata gcc ctg tgc ggc ttc tgc ttt cac   502
Leu Gly Ala Leu Gly Asn Gly Ile Ala Leu Cys Gly Phe Cys Phe His
                40   45   50

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atg aag acc tgg aag tca agc act att tac ctt ttc aac ttg gct gtg   550
Met Lys Thr Trp Lys Ser Ser Thr Ile Tyr Leu Phe Asn Leu Ala Val
             55                  60                  65

gcc gat ttt ctc ctc atg atc tgc tta ccc ctt cgg aca gac tac tac   598
Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Leu Arg Thr Asp Tyr Tyr
         70                  75                  80

ctc aga cgc aga cac tgg att ttt gga gat atc gcc tgt cgc ctg gtc   646
Leu Arg Arg Arg His Trp Ile Phe Gly Asp Ile Ala Cys Arg Leu Val
     85                  90                  95

ctc ttc aag ctg gcc atg aat agg gcc ggg agc att gtc ttc ctc act   694
Leu Phe Lys Leu Ala Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr
100                 105                 110                 115

gtg gtg gct gtg gat agg tat ttc aaa gtg gtc cac ccc cac cat atg   742
Val Val Ala Val Asp Arg Tyr Phe Lys Val Val His Pro His His Met
                120                 125                 130

gtg aat gcc atc tcc aac cgg act gcc gcc gcc acc gcc tgt gtc ctc   790
Val Asn Ala Ile Ser Asn Arg Thr Ala Ala Ala Thr Ala Cys Val Leu
            135                 140                 145

tgg act ttg gtc atc ttg ggg act gtg tat ctt ctg atg gag agt cac   838
Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Met Glu Ser His
        150                 155                 160

ctg tgt gtg cag ggg aca ctg tcg tcc tgt gag agc ttc atc atg gag   886
Leu Cys Val Gln Gly Thr Leu Ser Ser Cys Glu Ser Phe Ile Met Glu
    165                 170                 175

tca gcc aac ggg tgg cac gat gtc atg ttc cag ctg gag ttc ttc ctg   934
Ser Ala Asn Gly Trp His Asp Val Met Phe Gln Leu Glu Phe Phe Leu
180                 185                 190                 195

ccc ctg aca atc atc ttg ttc tgc tcg gtc aac gtt gtt tgg agc ctg   982
Pro Leu Thr Ile Ile Leu Phe Cys Ser Val Asn Val Val Trp Ser Leu
                200                 205                 210

aga cgg agg cag cag ctg acc aga cag gct cgg atg agg agg gcc acc   1030
Arg Arg Arg Gln Gln Leu Thr Arg Gln Ala Arg Met Arg Arg Ala Thr
            215                 220                 225

cgg ttc atc atg gtg gtg gct tct gtg ttc atc acg tgt tac ctg ccc   1078
Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr Cys Tyr Leu Pro
        230                 235                 240

agc gtg ctg gct agg ctc tac ttc ctc tgg acg gtg ccc act agt gcc   1126
Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val Pro Thr Ser Ala
    245                 250                 255

tgt gac ccc tct gtc cac aca gcc ctc cac gtc acc ctg agc ttc acc   1174
Cys Asp Pro Ser Val His Thr Ala Leu His Val Thr Leu Ser Phe Thr
260                 265                 270                 275

tac ctg aac agt atg ctg gat ccc ctt gta tat tac ttc tca agc ccc   1222
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Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro
                280                 285                 290

tcg ctc ccc aaa ttc tac gcc aag ctc aca atc tgc agc ctg aag ccc   1270
Ser Leu Pro Lys Phe Tyr Ala Lys Leu Thr Ile Cys Ser Leu Lys Pro
            295                 300                 305

aaa cgc cca gga cgc acg aag acg cgg agg tca gaa gag atg cca att   1318
Lys Arg Pro Gly Arg Thr Lys Thr Arg Arg Ser Glu Glu Met Pro Ile
        310                 315                 320

tcg aac ctc tgc agt aag agc tcc atc gat ggg gca aat cgt tcc cag   1366
Ser Asn Leu Cys Ser Lys Ser Ser Ile Asp Gly Ala Asn Arg Ser Gln
    325                 330                 335

agg cca tct gac ggg cag tgg gat ctc caa gtg tgt tgaatgccat        1412
Arg Pro Ser Asp Gly Gln Trp Asp Leu Gln Val Cys
340                 345                 350

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tggaggactt gaagatgtcc cctcccactc ttagctgtat ctttctcact caggtagaaa 1532

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ccagggaagg gaccttgaca tttatgtcta aagacataaa ttagatgctc ctcaaggttg 2732

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ttaatgcaat aaaaatttta ttggctacac ggtcaagttt gaatcttagt ttaaatgctt 3032

attagacatg tgctcgtagg gaagacttta tttaacccca ctcagttttg atgttcagca 3092

gggttaatac tgatgccaaa gggtttggga gcaaattcaa tgactgtaca ctcataagca 3152

tgagaaatct gttgttccca ggtctgcccg gaagaagacc atgtgcgtgt agtagttgat 3212

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Val Phe Val Leu Gly Ala Leu Gly Asn Gly Ile Ala Leu Cys Gly Phe
         35                  40                  45

Cys Phe His Met Lys Thr Trp Lys Ser Ser Thr Ile Tyr Leu Phe Asn
     50                  55                  60

Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Leu Arg Thr
 65                  70                  75                  80

Asp Tyr Tyr Leu Arg Arg Arg His Trp Ile Phe Gly Asp Ile Ala Cys
                 85                  90                  95

Arg Leu Val Leu Phe Lys Leu Ala Met Asn Arg Ala Gly Ser Ile Val
            100                 105                 110

Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Lys Val Val His Pro
        115                 120                 125

His His Met Val Asn Ala Ile Ser Asn Arg Thr Ala Ala Ala Thr Ala
    130                 135                 140
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Cys Val Leu Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Met
145                 150                 155                 160

Glu Ser His Leu Cys Val Gln Gly Thr Leu Ser Ser Cys Glu Ser Phe
                165                 170                 175

Ile Met Glu Ser Ala Asn Gly Trp His Asp Val Met Phe Gln Leu Glu
            180                 185                 190

Phe Phe Leu Pro Leu Thr Ile Ile Leu Phe Cys Ser Val Asn Val Val
        195                 200                 205

Trp Ser Leu Arg Arg Arg Gln Gln Leu Thr Arg Gln Ala Arg Met Arg
    210                 215                 220

Arg Ala Thr Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr Cys
225                 230                 235                 240

Tyr Leu Pro Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val Pro
                245                 250                 255

Thr Ser Ala Cys Asp Pro Ser Val His Thr Ala Leu His Val Thr Leu
            260                 265                 270

Ser Phe Thr Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr Phe
        275                 280                 285

Ser Ser Pro Ser Leu Pro Lys Phe Tyr Ala Lys Leu Thr Ile Cys Ser
    290                 295                 300

Leu Lys Pro Lys Arg Pro Gly Arg Thr Lys Thr Arg Arg Ser Glu Glu
305                 310                 315                 320

Met Pro Ile Ser Asn Leu Cys Ser Lys Ser Ser Ile Asp Gly Ala Asn
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Arg Ser Gln Arg Pro Ser Asp Gly Gln Trp Asp Leu Gln Val Cys
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agacccccaa gctgcagcct ggcaatgtac gcttttggaa aactgctctc gcctcagagc 180

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agaaaggacc tgctgtcggc tttcatttcc tgactgaagt tgggtgatga ggttaggggc 300

ccagctgcca aggggaacca tagtgttcag ataggcagct gtgcctttgt gtcagccacc 360

tagg atg ctc ttc ctc tct ccg agt gct atg gac aac ggg tcg tgc tgt  409
     Met Leu Phe Leu Ser Pro Ser Ala Met Asp Asn Gly Ser Cys Cys
       1               5                  10                  15

ctc atc gag ggg gaa ccc atc acc cag gta atg cca cct tta ctc atc   457
Leu Ile Glu Gly Glu Pro Ile Thr Gln Val Met Pro Pro Leu Leu Ile
                20                  25                  30

ctg gcc ttc ctg ctt gga gcc ctg ggc aac ggc cta gcc ctg tgt ggt   505
Leu Ala Phe Leu Leu Gly Ala Leu Gly Asn Gly Leu Ala Leu Cys Gly
            35                  40                  45

ttc tgc ttt cac atg aag acc tgg aag tcg agc act att tac ctt ttc   553
Phe Cys Phe His Met Lys Thr Trp Lys Ser Ser Thr Ile Tyr Leu Phe
        50                  55                  60

aac ttg gct gta gcc gat ttt ctc ctc atg atc tgc cta ccc ctt cgg   601
Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Leu Arg
    65                  70                  75

aca gac tac tac ctc aga cgt agg cat tgg att ttg ggg gat att ccc   649
Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ile Leu Gly Asp Ile Pro
80                  85                  90                  95

tgc cgc ctg gtc ctc ttc atg ctg gcc atg aat agg gcc gga agc att   697
Cys Arg Leu Val Leu Phe Met Leu Ala Met Asn Arg Ala Gly Ser Ile
                100                 105                 110

gtc ttc ctc act gtg gtg gcc gtg gac agg tat ttc aaa gtg gtc cac   745
Val Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Lys Val Val His
            115                 120                 125

ccc cac cat atg gtg aac gcc atc tcc aat cgg act gca gct gcc atc   793
Pro His His Met Val Asn Ala Ile Ser Asn Arg Thr Ala Ala Ala Ile
        130                 135                 140

gtc tgt gtc ctc tgg act ttg gtc atc ttg ggg act gtg tat ctt ctg   841
Val Cys Val Leu Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu
    145                 150                 155

atg gag agt cac ctg tgt gtg cgg ggg atg gtg tca tct tgt gag agc   889
Met Glu Ser His Leu Cys Val Arg Gly Met Val Ser Ser Cys Glu Ser
160                 165                 170                 175

ttc atc atg gag tca gcc aac ggg tgg cac gat atc atg ttc cag ctg   937
Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met Phe Gln Leu
                180                 185                 190

gag ttc ttc ctg ccc ctg acc atc atc ttg ttc tgc tcc ttc aaa gtt   985
Glu Phe Phe Leu Pro Leu Thr Ile Ile Leu Phe Cys Ser Phe Lys Val
            195                 200                 205
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Val Trp Ser Leu Arg Gln Arg Gln Gln Leu Thr Arg Gln Ala Arg Met
        210                 215                 220

agg agg gcc acc cgg ttc atc atg gtg gtg gct tcc gtg ttc atc acg   1081
Arg Arg Ala Thr Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr
    225                 230                 235

tgt tac ctg ccc agc gtg ttg gcg agg ctc tac ttc ctc tgg acg gtg   1129
Cys Tyr Leu Pro Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val
240                 245                 250                 255

ccc tcc agt gct tgt gac ccc tct gtc cac ata gct ctc cat gtc acc   1177
Pro Ser Ser Ala Cys Asp Pro Ser Val His Ile Ala Leu His Val Thr
                260                 265                 270

ctg agt ctc acc tac ctg aac agc atg ctg gac cct ctt gtg tac tac   1225
Leu Ser Leu Thr Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr
            275                 280                 285

ttt tca agc ccc tcg ttc ccc aaa ttc tac gcc aag ctc aaa atc cgc   1273
Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Ala Lys Leu Lys Ile Arg
        290                 295                 300

agc ttg aaa ccc aga cgc cca gga cgc tcg cag gca cgg agg tcg gaa   1321
Ser Leu Lys Pro Arg Arg Pro Gly Arg Ser Gln Ala Arg Arg Ser Glu
    305                 310                 315

gag atg cca att tcg aat ctc tgt cgt aag agt tcc acc gat gtg gta   1369
Glu Met Pro Ile Ser Asn Leu Cys Arg Lys Ser Ser Thr Asp Val Val
320                 325                 330                 335

aat agt tcc cag agg ccg tct gac ggg cag tgg ggt ctc caa gtg tgt   1417
Asn Ser Ser Gln Arg Pro Ser Asp Gly Gln Trp Gly Leu Gln Val Cys
                340                 345                 350

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aatctgaagg gtgagggact tgaaaaatga cagccccccc cccccgccca cccgcccgcc 1537

cgccccgctc tttctcagct gtgtctttct cactcaagta gaagcaaaat ctaaaaaaaa 1597

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<213> Rattus norvegicus

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            20                  25                  30

Ala Phe Leu Leu Gly Ala Leu Gly Asn Gly Leu Ala Leu Cys Gly Phe
        35                  40                  45

Cys Phe His Met Lys Thr Trp Lys Ser Ser Thr Ile Tyr Leu Phe Asn
    50                  55                  60

Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Leu Arg Thr
65                  70                  75                  80

Asp Tyr Tyr Leu Arg Arg Arg His Trp Ile Leu Gly Asp Ile Pro Cys
                85                  90                  95

Arg Leu Val Leu Phe Met Leu Ala Met Asn Arg Ala Gly Ser Ile Val
            100                 105                 110

Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Lys Val Val His Pro
        115                 120                 125

His His Met Val Asn Ala Ile Ser Asn Arg Thr Ala Ala Ala Ile Val
    130                 135                 140

Cys Val Leu Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Met
145                 150                 155                 160

Glu Ser His Leu Cys Val Arg Gly Met Val Ser Ser Cys Glu Ser Phe
                165                 170                 175

Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met Phe Gln Leu Glu
            180                 185                 190

Phe Phe Leu Pro Leu Thr Ile Ile Leu Phe Cys Ser Phe Lys Val Val
        195                 200                 205

Trp Ser Leu Arg Gln Arg Gln Gln Leu Thr Arg Gln Ala Arg Met Arg
    210                 215                 220

Arg Ala Thr Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr Cys
225                 230                 235                 240

Tyr Leu Pro Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val Pro
                245                 250                 255

Ser Ser Ala Cys Asp Pro Ser Val His Ile Ala Leu His Val Thr Leu
            260                 265                 270

Ser Leu Thr Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr Phe
        275                 280                 285

Ser Ser Pro Ser Phe Pro Lys Phe Tyr Ala Lys Leu Lys Ile Arg Ser
    290                 295                 300

Leu Lys Pro Arg Arg Pro Gly Arg Ser Gln Ala Arg Arg Ser Glu Glu
305                 310                 315                 320
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Met Pro Ile Ser Asn Leu Cys Arg Lys Ser Ser Thr Asp Val Val Asn
325 330 335

Ser Ser Gln Arg Pro Ser Asp Gly Gln Trp Gly Leu Gln Val Cys
340 345 350

<210> 7
<211> 15
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 7
Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10 15

<210> 8
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: internalizing domain derived from HIV tat protein

<400> 8
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 9
aagaggacca ggcggcaggg aatat 25

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 10
tatcccccaa aatccaatgc ctacg 25

<210> 11
<211> 24

<212> DNA
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<220>
<223> Description of Artificial Sequence: forward primer

<400> 11
cgggcaggtg ggtgatgagg ttag 24

<210> 12
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: reverse primer

<400> 12
gctgctgggc catttgtctt cat 23

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 13
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<210> 14
<211> 21
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 14
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<210> 15
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 15

cctcctcatc cgagcctgtc tgg 23

<210> 16
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<400> 16
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<210> 17
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<400> 17
ttcacgttgg ccatgaaca 19

<210> 18
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 18
aaatacctgt ccgcagcc 18

<210> 19
<211> 24
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<400> 19
ccgtaaggaa cacgatgctc ccgg 24

<210> 20
<211> 15
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<400> 20
gtcgacggcg agccc 15

<210> 21
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 21
tctttgggac cttgtctgc 19

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide probe

<400> 22
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